



Db 103 SKCRKMNQVEISPTVYVDVTCGCRKNQRYFWSEITLFCNNCSLNGTVOISCOEQ 162  
 QY 123 NVVCTCHAGFFLRNFCVSCNCKS 148  
 Db 163 NTICTCHAGFFLRNFCVSCNCKN 188

## RESULT 2

Q95185 ID Q95185 PRELIMINARY; PRT; 189 AA.  
 AC Q95185  
 DT 01-FEB-1997 (Tremblrel. 02, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).  
 GN TNFR\_1  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia, Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RA Duthie S., Nasir L., Ekersall P.D.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: 072344; AAB95089.1; -;  
 DR HSSP: P19438; 1RXI.  
 DR InterPro: IPR000561; EGF-like.  
 DR Pfam: PF00020; TNFR\_C6; 3.  
 DR ProDom: PD000771; TNFR\_C6; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00050; TNFR\_NGFR\_2; 3.  
 FT NON\_TER 189 189  
 SQ SEQUENCE 189 AA: 21420 MW: 717680; P804070E CR664;

Query Match 77.7%; Score 731; DB 6; Length 189;  
 Best Local Similarity 85.5%; Pred. No. 1,7c 68;  
 Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0;  
 QY 4 CPQGYIHFQNNISLCTKCHKYTYLYNCPGQGTDTWRETESGSFTASENHILRHCLSCS 63  
 Db 44 CPQGYIHFQNNISLCTKCHKYTYLYNCPGQGTDTWRETESGSFTASENHILRHCLSCS 103  
 QY 64 KCRKMGCGVEISSSTVLKDTWTPGPKNYRHYWSENLFQFNCSLNLNFTVHLSSGPKQN 123  
 Db 104 KCRKMGCGVEISSSTVLKDTWTPGPKNYRHYWSENLFQFNCSLNLNFTVHLSSGPKQN 163  
 QY 124 IVCTCHAGFFLRNFCVSCNCKS 148  
 Db 164 TVCTCHAGFFLRNFCVSCVNVNKKN 188

## RESULT 3

Q99MM1 ID Q99MM1 PRELIMINARY; PRT; 413 AA.  
 AC Q99MM1  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE WSL-1-LIKE PROTEIN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-129/SV;  
 RX MEDLINE-21158384; Pubmed 11261933;  
 RA Wang E.C.Y., Kittson J., Thirn A., Williams J., Farrow S.N.,

RA Owen M.J.;  
 RT "Genomic structure, expression, and chromosome mapping of the mouse  
 RT homologue for the WSL-1 (WSL1, Apo3, TRAMP, IAPB, IR3, TNFRSF12)  
 RT gene.";  
 RL Immunogenetics 53:59-63(2001).  
 DR EMBL: AF329969; AAK11256.1; -;  
 SQ SEQUENCE 413 AA: 44453 MW: 69F21B85D0DABAF CR664;

Query Match 21.5%; Score 202; DB 11; Length 413;  
 Best Local Similarity 31.4%; Pred. No. 2,6c-13;  
 Matches 48; Conservative 19; Mismatches 58; Indels 28; Gaps 7;  
 QY 18 CTCTKCHKYTYLYNCPGQGTDTWRETESGSFTASENHILRHCLSCSKCKEMCGVEISS 76  
 Db 54 CTCTKCHKYTYLYNCPGQGTDTWRETESGSFTASENHILRHCLSCSKCKEMCGVEISS 113  
 QY 77 CTVDRTVCGCRKNQRYHYWSENLFQFNCSLNLNFTVHLSC-----QEKONTVCT 127  
 Db 114 CSAKSLIHGGRQSG-----W-----CVKSTVPCGKSSFSVPGGATTFVHEATPPRP 162  
 QY 128 CHAGFFLRNFCVSC-----SNCKKSLCTKIC 155  
 Db 163 CLPFPYIRGNDCTSCPTGFSVCPKA--CTAVC 193

## RESULT 4

Q9ER63 ID Q9ER63 PRELIMINARY; PRT; 147 AA.  
 AC Q9ER63  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR P60 HOMOLOGUE 1.  
 GN TNFRSF1A1 OR TNFRH1  
 OS Mus musculus domesticus (western European house mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10092;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-129 SV;  
 RX MEDLINE-20519229; Pubmed 11063728;  
 RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,  
 RA Lane N., Reik W., Walter J.;  
 RT "Sequence and functional comparison in the Beckwith-Wiedemann region:  
 RT implications for a novel imprinting centre and extended imprinting.";  
 RL Hum. Mol. Genet. 9:2691-2706(2000)  
 RN 121  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-129 SV;  
 RL Engemann S.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A1278264; CAC16405.1; -;  
 DR EMBL: A1278505; CAC27352.1; -;  
 DR MGD: MGI:1930269; Tnfrsf1a1.  
 DR InterPro: IPR000345; Cyt\_c\_heme\_bind.  
 DR InterPro: IPR001368; TNFR\_C6; 3.  
 DR Pfam: PF00020; TNFR\_C6; 3.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00140; CYT\_C\_HEME\_C; UNKNOWN\_1.  
 DR PROSITE: PS00050; TNFR\_NGFR\_2; 2.  
 KW Receptor.  
 SQ SEQUENCE 147 AA: 16253 MW: 76442714455170C9 CR664;

Query Match 21.3%; Score 200.5; DB 11; Length 147;  
 Best Local Similarity 33.6%; Pred. No. 1,6c-13;  
 Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps 4;  
 QY 4 CPQGYIHFQNNISLCTKCHKYTYLYNCPGQGTDTWRETESGSFTASENHILRHCLSCS 63  
 Db 44 CPQGYIHFQNNISLCTKCHKYTYLYNCPGQGTDTWRETESGSFTASENHILRHCLSCS 103



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Query Match      21.3%; Score 200.5; DB 4; Length 418;
Best Local Similarity 29.8%; Pred. No. 37e-13;
Matches 48; Conservative 29; Mismatches 72; Indels 21; Gaps 7;

QY 11 HPNNSTGCKIKHKGKLYLYNAGGQDIDCKECSGFIASENHLEK-HGHSCKSKCKEM 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 40 HKKIGLEFCGRCGPAHYIKAKPTKPGNSD-LV-PQDTFLAWENHNSB-AKQUN-DEQA 99
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 70 GQVEISSCTVDPTGCTGKNGYPIHYWSENFQ-----FN-SLP-LN-GTVH-----LSVQ 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 100 SQVALPNCASAVADTCGCKGKQFWFVLC-----QVSQCVSSSPFYQDCLDAGLHRRHKLICS 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 120 EKGNTVCTGACGFFLENECVSC --SNCKKSLECKLC 155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 PRTDGTGCLPGFYHNGGQVSCPTSTLCSGP--PCANVC 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
ID Q9ER62 PRELIMINARY; PRT: 141 AA.
AC Q9ER62:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2001 (TrEMBLrel. 16, Last sequence update)
DE TUMOR NECROSIS FACTOR PROTECTOR p60 HOMOLOGUE 2
GN TNFRSF1A2 OR TNFR12.
OS Mus musculus domesticus (western European house mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Strodick M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT Implications for a novel imprinting centre and extended imprinting."
RL Hum. Mol. Genet. 9:2691-2706(2000);
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX Engemann S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases
DP EMBL: AJ278265; CAC16406 1.
DR EMBL: AJ276505; CAC27353.1; -.
DR MGI: MGI:1930270; Tnfrsf1a2.
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR001368; TNFR_C6.
DR Plan: PF00020; TNFR_C6; 3.
DP SMART: SM00208; TNFR; 3.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 141 AA; 15576 MW; 7552DE3E8A8E5F3 CRC64;

Query Match      21.1%; Score 198.5; DB 11; Length 141;
Best Local Similarity 32.8%; Pred. No. 2.5e-13;
Matches 41; Conservative 18; Mismatches 59; Indels 7; Gaps 4;

QY 4 CQCKYIHPGNNSTGCKIKHKGKLYLYNAGGQDIDCKECSGFIASENHLEK-HGHSCKSKCKEM 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9 CQAGEY---WSKDVCCNCSAGTEVKAPCEIPHTGQCKECPHTFTEKQNYLQACILCS 65
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 64 KCKHMGQVEISSCTVDPTGCTGKNGYPIHYWSENFQ-----FN-SLP-LN-GTVH-----LSVQ 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66 ICCKD--QFWVAUCSATSURKCKGCKGKLYLYNAGGQDIDCKECSGFIASENHLEK-HGHSCKSKCKEM 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 123 NTVCT 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 162 NTVCS 166

RESULT 10
Q9BY86 PRELIMINARY; PRT: 417 AA.
ID Q9BY86:
AC Q9BY86:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DB 123 NTVCS 127

RESULT 9
Q9CZA4 PRELIMINARY; PRT: 180 AA.
ID Q9CZA4:
AC Q9CZA4:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 24082806ATK PROTEIN.
GN TNFRSF1A2 OR 2810028K06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57H1/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Akawa K., Iwawa M., Nishi K., Miyasawa H., Kondo S., Yamada A.,
RA Saito T., Okazaki Y., Gajobori T., Hono H., Kusukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Rafalow S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaid T., Pevsler J., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki K., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Anno H., Baldarelli P., Barsh G.,
RA Hlake J., Hoffell D., Hozumi N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Holt C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ping R., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tayaoka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Burke A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
PL Nature 409:685-690(2001).
DR EMBL: AK012838; BAB28502.1; -.
DR MGI: MGI:1930270; Tnfrsf1a2.
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR001368; TNFR_C6.
DR Plan: PF00020; TNFR_C6; 3.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 180 AA; 20226 MW; F8F56F165AD053FA CRC64;

Query Match      21.1%; Score 198.5; DB 11; Length 180;
Best Local Similarity 32.8%; Pred. No. 3e-13;
Matches 41; Conservative 18; Mismatches 59; Indels 7; Gaps 4;

QY 4 CQCKYIHPGNNSTGCKIKHKGKLYLYNAGGQDIDCKECSGFIASENHLEK-HGHSCKSKCKEM 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 48 CQAGEY---WSKDVCCNCSAGTEVKAPCEIPHTGQCKECPHTFTEKQNYLQACILCS 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 64 KCKHMGQVEISSCTVDPTGCTGKNGYPIHYWSENFQ-----FN-SLP-LN-GTVH-----LSVQ 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 105 ICCKD--QFWVAUCSATSURKCKGCKGKLYLYNAGGQDIDCKECSGFIASENHLEK-HGHSCKSKCKEM 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 123 NTVCT 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 162 NTVCS 166

RESULT 10
Q9BY86 PRELIMINARY; PRT: 417 AA.
ID Q9BY86:
AC Q9BY86:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RA Chaudhary P.M., Hood L.E.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBST databases.  
 DR EMBL; U83598; AA041433.1; -;  
 DR HSSP; P19438; TEXT.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6;  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00208; TNFR\_2.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
 KW Receptor.  
 FT NON\_TER  
 ST SEQUENCE 175 AA: 18634 MW: 46468756832157 GP064;

Query Match 20.8%; Score 196; DB 4; Length 175;  
 Best Local Similarity 31.5%; Pred. No. 5,4e-13;  
 Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;

QY 11 HPNNNSICCTKCHKCTYLYNDPGQDTCRCESGSETASENHLR-HCLSCSKCKKEM 69  
 DB 34 HKKIGLFCCKGCPACHYIKAPCTEPGCGNSTCLVPGDTFLAWENHNSKCAKCAQADGA 93  
 QY 70 GQVFISSTVDRDVTGCKKQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSQ 119  
 DB 94 SQVALENCSAVALTRGCKRGWFEV-----QVSCVSSSPFYQCLDQALHRIKLQS 150  
 QY 120 EKQNTVCTCHAGFFLENKVCSC 142  
 DB 151 KRDTGCTCLPGFYRHGDCVSC 173

## RESULT 14

Q9UMF0  
 ID Q9UMF0 PRELIMINARY; PRT: 178 AA.  
 AC Q9UMF0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 11 (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RA Secretion G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,  
 RA McMichael A.J., Bell J.L.;  
 RL "LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing."  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
 DR EMBL; U94512; AAC51316.1; -;  
 DR HSSP; P19438; TEXT.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6;  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00208; TNFR\_2.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
 KW Receptor.  
 FT NON\_TER  
 ST SEQUENCE 178 AA: 19043 MW: 474686B96BFB19F4 CR064;

Query Match 20.8%; Score 196; DB 4; Length 178;  
 Best Local Similarity 31.5%; Pred. No. 5,5e-13;  
 Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;  
 QY 11 HPNNNSICCTKCHKCTYLYNDPGQDTCRCESGSETASENHLR-HCLSCSKCKKEM 69  
 DB 37 HKKIGLFCCKGCPACHYIKAPCTEPGCGNSTCLVPGDTFLAWENHNSKCAKCAQADGA 96  
 QY 70 GQVFISSTVDRDVTGCKKQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSQ 119  
 DB 97 SQVALENCSAVALTRGCKRGWFEV-----QVSCVSSSPFYQCLDQALHRIKLQS 153  
 QY 120 EKQNTVCTCHAGFFLENKVCSC 142  
 DB 154 KRDTGCTCLPGFYRHGDCVSC 176

## RESULT 15

Q9UMF1  
 ID Q9UMF1 PRELIMINARY; PRT: 181 AA.  
 AC Q9UMF1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RA Secretion G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,  
 RA McMichael A.J., Bell J.L.;  
 RL "LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing."  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
 DR EMBL; U94505; AAC51310.1; -;  
 DR HSSP; P19438; TEXT.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6;  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00208; TNFR\_2.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
 KW Receptor.  
 ST SEQUENCE 181 AA: 13432 MW: 59AAFE5B646E969 CR064;

Query Match 20.8%; Score 196; DB 4; Length 181;  
 Best Local Similarity 31.5%; Pred. No. 5,5e-13;  
 Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;  
 QY 11 HPNNNSICCTKCHKCTYLYNDPGQDTCRCESGSETASENHLR-HCLSCSKCKKEM 69  
 DB 40 HKKIGLFCCKGCPACHYIKAPCTEPGCGNSTCLVPGDTFLAWENHNSKCAKCAQADGA 99  
 QY 70 GQVFISSTVDRDVTGCKKQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSQ 119  
 DB 100 SQVALENCSAVALTRGCKRGWFEV-----QVSCVSSSPFYQCLDQALHRIKLQS 156  
 QY 120 EKQNTVCTCHAGFFLENKVCSC 142  
 DB 157 KRDTGCTCLPGFYRHGDCVSC 179

Search completed: April 24, 2002, 10:46:49  
 Job time: 617 sec



